



SEQUENCE LISTING

<110> Sunol Molecular Corporatiopn
Sherman, Linda
Lustgarten, Joseph

<120> RECOMBINANT CONSTRUCTS ENCODING T CELL
RECEPTORS SPECIFIC FOR HUMAN HLA-RESTRICTED TUMOR ANTIGENS

<130> 31333-20001.01

<140> US 09/774,681

<141> 2001-02-01

<150> US 08/812,393

<151> 1997-03-05

<150> US 60/012,845

<151> 1996-03-05

<160> 65

<170> FastSEQ for Windows Version 4.0

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<223> Polynucleotide derivative of effective T cell
receptor

<221> CDS

<222> (1)...(1350)

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Leu	Glu	Met	Gln	Arg	Asn	Leu	Gly	Ala	Val	Leu	Gly	Ile	Leu	Trp	Val	
1			5					10						15		

cag	att	tgc	tgg	ctg	aaa	gaa	cag	caa	gtg	cag	cag	agt	ccc	gca	tcc	96
Gln	Ile	Cys	Trp	Leu	Lys	Glu	Gln	Gln	Val	Gln	Gln	Ser	Pro	Ala	Ser	
		20					25						30			

ttg	gtt	ctg	cag	gag	ggg	gag	aac	gca	gag	ctc	cag	tgt	agc	ttt	tcc	144
Leu	Val	Leu	Gln	Glu	Gly	Glu	Asn	Ala	Glu	Leu	Gln	Cys	Ser	Phe	Ser	
		35				40					45					

atc	ttt	aca	aac	cag	gtg	cag	tgg	ttt	tac	caa	cgt	cct	ggg	gga	aga	192
Ile	Phe	Thr	Asn	Gln	Val	Gln	Trp	Phe	Tyr	Gln	Arg	Pro	Gly	Gly	Arg	
		50				55					60					

ctc	gtc	agc	ctg	ttg	tac	aat	cct	tct	ggg	aca	aag	cag	agt	ggg	aga	240
Leu	Val	Ser	Leu	Leu	Tyr	Asn	Pro	Ser	Gly	Thr	Lys	Gln	Ser	Gly	Arg	

65	70	75	80	
ctg aca tcc aca aca gtc att aaa gaa cgt cgc agc tct ttg cac att				288
Leu Thr Ser Thr Thr Val Ile Lys Glu Arg Arg Ser Ser Leu His Ile				
	85	90	95	
tcc tcc tcc cag atc aca gac tca ggc act tat ctc tgt gcc tca aat				336
Ser Ser Ser Gln Ile Thr Asp Ser Gly Thr Tyr Leu Cys Ala Ser Asn				
	100	105	110	
tct gga gga agc aat gca aag cta acc ttc ggg aaa ggc act aaa ctc				384
Ser Gly Gly Ser Asn Ala Lys Leu Thr Phe Gly Lys Gly Thr Lys Leu				
	115	120	125	
tct gtt aaa tca ggt ggc gga ggg tct ggc ggg ggt gga tcc ggg ggt				432
Ser Val Lys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly				
	130	135	140	
gga ggc tca gag gct gca gtc acc caa agc cca aga aac aag gtg gca				480
Gly Gly Ser Glu Ala Ala Val Thr Gln Ser Pro Arg Asn Lys Val Ala				
	145	150	155	160
gta aca gga gga aag gtg aca ttg agc tgt aat cag act aat aac cac				528
Val Thr Gly Gly Lys Val Thr Leu Ser Cys Asn Gln Thr Asn Asn His				
	165	170	175	
aac aac atg tac tgg tat cgg cag gac acg ggg cat ggg ctg agg ctg				576
Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu				
	180	185	190	
atc cat tat tca tat ggt gct ggc agc act gag aaa gga gat atc cct				624
Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr Glu Lys Gly Asp Ile Pro				
	195	200	205	
gat gga tac aag gcc tcc aga cca agc caa gag aac ttc tcc ctc att				672
Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile				
	210	215	220	
gtg gag ttg ggt acc ccc tct cag aca tca gtg tac ttc tgt gcc agc				720
Val Glu Leu Gly Thr Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser				
	225	230	235	240
ggt gag aca ggg acc aac gaa aga tta ttt ttc ggt cat gga acc aag				768
Gly Glu Thr Gly Thr Asn Glu Arg Leu Phe Phe Gly His Gly Thr Lys				
	245	250	255	
ctg tct gtc ctg act agt aac tcc atc atg tac ttc agc cac ttc gtg				816
Leu Ser Val Leu Thr Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val				
	260	265	270	
ccg gtc ttc ctg cca gcg aag ccc acc acg acg cca gcg ccg cga cca				864
Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro				
	275	280	285	
cca aca ccg gcg ccc acc atc gcg tcg cag ccc ctg tcc ctg cgc cca				912
Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro				
	290	295	300	

tct agt tct aga gat ccc aaa ctc tgc tac ctg ctg gat gga atc ctc	960
Ser Ser Ser Arg Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu	
305 310 315 320	
ttc atc tat ggt gtc att ctc act gcc ttg ttc ctg aga gtg aag ttc	1008
Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe	
325 330 335	
agc agg agc gca gac gcc ccc gcg tac cag cag ggc cag aac cag ctc	1056
Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu	
340 345 350	
tat aac gag ctc aat cta gga cga aga gag gag tac gat gtt ttg gac	1104
Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp	
355 360 365	
aag aga cgt ggc cgg gac cct gag atg ggg gga aag ccg aga agg aag	1152
Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys	
370 375 380	
aac cct cag gaa ggc ctg tac aat gaa ctg cag aaa gat aag atg gcg	1200
Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala	
385 390 395 400	
gag gcc tac agt gag att ggg atg aaa ggc gag cgc cgg agg ggc aag	1248
Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys	
405 410 415	
ggg cac gat ggc ctt tac cag ggt ctc agt aca gcc acc aag gac acc	1296
Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr	
420 425 430	
tac gac gcc ctt cac atg cag gcc ctg ccc cct cgc taa gcg gcc gcc	1344
Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg * Ala Ala Ala	
435 440 445	
acc gcg	1350
Thr Ala	

<210> 2
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<220>
 <223> Deduced amino acid derivative of effective T cell
 receptor

<400> 2
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 1 5 10 15
 Gln Ile Cys Trp Leu Lys Glu Gln Gln Val Gln Gln Ser Pro Ala Ser
 20 25 30
 Leu Val Leu Gln Glu Gly Glu Asn Ala Glu Leu Gln Cys Ser Phe Ser

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<223> Primer

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cccaaggcac tgatgttcat cttc

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<212> DNA

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<220>

<223> Primer

<400> 4

tgagacaaag tccccaatct ctgacag

27

<210> 5

<211> 26

<212> DNA

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<220>

<223> Primer

<400> 5

ctgcagctgc tcctcaagta ctattc

26

<210> 6

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 6

tcccggagaa ggtccacagt tcctcttt

28

<210> 7

<211> 29

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<220>

<223> Primer

<400> 7

gaagcagcag aggggttgaa gccacatac

29

<210> 8

<211> 27

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<220>
<223> Primer

<400> 8
ggcaggtctt cagttgctta tgaaggt

27

<210> 9
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<220>
<223> Primer

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ggttcctctt cagcgtccag aatatgt

27

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<220>
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gcgaagaact caccctggac tgttcat

27

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<220>
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<400> 11
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30

<210> 12
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<400> 12
gagctgcgac gttccttagt gactgtg

27

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<400> 18

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gtgtatgaaa cccaggacag ttcttac

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<223> Primer

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<210> 22

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<400> 23

atctaattct gggaagagca aat

23

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ggcgtctggg accacgtggg caa

23

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gtgaaagggc aaggacaaaa agc

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gatatgcgaa cagtatctag gc

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acataatcaa aggaaaggga gaa

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tcctgattgg tcacgaaggg caa

23

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<400> 33
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gattatgttt agctacaata ata

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<210> 35
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<400> 35
acaaggtgac agggaaggga caa

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<210> 36
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<400> 36
acctacagaa cccaaggact cag

23

<210> 37
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<400> 37
cagttgccct cgatcgatt ttc

23

<210> 38
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<400> 38
gccgagatca aggctgtggg cag

23

<210> 39
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<220>

<223> Primer

<400> 39

agaaccatct gtaagagtgg aac

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<210> 40

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<212> DNA

<213> Artificial Sequence

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<223> Primer

<400> 40

catcaaataa tagatatggg gca

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<210> 41

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 41

gtagtcctga aaaagggcac act

23

<210> 42

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 42

catctgtcaa agtggcactt ca

22

<210> 43

<211> 393

<212> DNA

<213> Artificial Sequence

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<223> Nucleotide sequence of the variable regions of the
alpha chain of H7-specific TCR

<221> CDS

<222> (1)...(393)

<400> 43

atg aaa tcc ttg agt gtt tcc cta gtg gtc ctg tgg ctc cag tta aac
Met Lys Ser Leu Ser Val Ser Leu Val Val Leu Trp Leu Gln Leu Asn
1 5 10 15

48

tgg gtg cag agc cag cag aag gtg cag cag agc cca gaa tcc ctc agt
Trp Val Gln Ser Gln Gln Lys Val Gln Gln Ser Pro Glu Ser Leu Ser

96

20	25	30	
gtc cca gag gga ggc atg gcc tct ctc aac tgc act tca agt gat cgc			144
Val Pro Glu Gly Gly Met Ala Ser Leu Asn Cys Thr Ser Ser Asp Arg			
35	40	45	
aat ttt cag tat ttc tgg tgg tac aga cag cat tct gga gaa ggc ccc			192
Asn Phe Gln Tyr Phe Trp Trp Tyr Arg Gln His Ser Gly Glu Gly Pro			
50	55	60	
aaa gca ctg atg tcc atc ttc tct gat ggt gac aag aaa gaa ggc aga			240
Lys Ala Leu Met Ser Ile Phe Ser Asp Gly Asp Lys Lys Glu Gly Arg			
65	70	75	80
ttc aca gct cac ctc aat aag gcc agc ctg cat gtt tcc ctg cac atc			288
Phe Thr Ala His Leu Asn Lys Ala Ser Leu His Val Ser Leu His Ile			
85	90	95	
aga gac tcc cag ccc agt gac tcc gct ctc tac ttc tgt gca gtt atg			336
Arg Asp Ser Gln Pro Ser Asp Ser Ala Leu Tyr Phe Cys Ala Val Met			
100	105	110	
gat tat aac cag ggg aag ctt atc ttt ggg cag ggt acc aag tta tct			384
Asp Tyr Asn Gln Gly Lys Leu Ile Phe Gly Gln Gly Thr Lys Leu Ser			
115	120	125	
atc aag ccc			393
Ile Lys Pro			
130			

<210> 44
 <211> 131
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of the variable regions of the
 alpha chain of H7-specific TCR

<400> 44
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 1 5 10 15
 Trp Val Gln Ser Gln Gln Lys Val Gln Gln Ser Pro Glu Ser Leu Ser
 20 25 30
 Val Pro Glu Gly Gly Met Ala Ser Leu Asn Cys Thr Ser Ser Asp Arg
 35 40 45
 Asn Phe Gln Tyr Phe Trp Trp Tyr Arg Gln His Ser Gly Glu Gly Pro
 50 55 60
 Lys Ala Leu Met Ser Ile Phe Ser Asp Gly Asp Lys Lys Glu Gly Arg
 65 70 75 80
 Phe Thr Ala His Leu Asn Lys Ala Ser Leu His Val Ser Leu His Ile
 85 90 95
 Arg Asp Ser Gln Pro Ser Asp Ser Ala Leu Tyr Phe Cys Ala Val Met
 100 105 110
 Asp Tyr Asn Gln Gly Lys Leu Ile Phe Gly Gln Gly Thr Lys Leu Ser
 115 120 125

Ile Lys Pro
130

<210> 45
<211> 402
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of the variable regions of the
beta chain of H7-specific TCR

<221> CDS
<222> (1)...(402)

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atg ggc tcc aga ctc ttc ttt gtg gtt ttg att ctc ctg tgt gca aaa 48
Met Gly Ser Arg Leu Phe Phe Val Val Leu Ile Leu Leu Cys Ala Lys
1 5 10 15

cac atg gag gct gca gtc acc caa agt cca aga agc aag gtg gca gta 96
His Met Glu Ala Ala Val Thr Gln Ser Pro Arg Ser Lys Val Ala Val
20 25 30

aca gga gga aag gtg aca ttg agc tgt cac cag act aat aac cat gac 144
Thr Gly Gly Lys Val Thr Leu Ser Cys His Gln Thr Asn Asn His Asp
35 40 45

tat atg tac tgg tat cgg cag gac acg ggg cat ggg ctg agg ctg atc 192
Tyr Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu Ile
50 55 60

cat tac tca tat gtc gct gac agc acg gag aaa gga gat atc cct gat 240
His Tyr Ser Tyr Val Ala Asp Ser Thr Glu Lys Gly Asp Ile Pro Asp
65 70 75 80

ggg tac aag gcc tcc aga cca agc caa gag aat ttc tct ctc att ctg 288
Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile Leu
85 90 95

gag ttg gct tcc ctt tct cag tca gct gta tat ttc tgt gcc agc agc 336
Glu Leu Ala Ser Leu Ser Gln Ser Ala Val Tyr Phe Cys Ala Ser Ser
100 105 110

gat ttc gcc ggg aca ggg ggc ttc tat gaa cag tac ttc ggt ccc ggc 384
Asp Phe Ala Gly Thr Gly Gly Phe Tyr Glu Gln Tyr Phe Gly Pro Gly
115 120 125

acc agg ctc acg gtt tct 402
Thr Arg Leu Thr Val Ser
130

<210> 46
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<213> Artificial Sequence

<220>

<223> Amino acid sequence of the variable regions of the
beta chain of H7-specific TCR

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Met	Gly	Ser	Arg	Leu	Phe	Phe	Val	Val	Leu	Ile	Leu	Leu	Cys	Ala	Lys
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His	Met	Glu	Ala	Ala	Val	Thr	Gln	Ser	Pro	Arg	Ser	Lys	Val	Ala	Val
		20					25					30			
Thr	Gly	Gly	Lys	Val	Thr	Leu	Ser	Cys	His	Gln	Thr	Asn	Asn	His	Asp
	35					40					45				
Tyr	Met	Tyr	Trp	Tyr	Arg	Gln	Asp	Thr	Gly	His	Gly	Leu	Arg	Leu	Ile
	50					55				60					
His	Tyr	Ser	Tyr	Val	Ala	Asp	Ser	Thr	Glu	Lys	Gly	Asp	Ile	Pro	Asp
65				70					75				80		
Gly	Tyr	Lys	Ala	Ser	Arg	Pro	Ser	Gln	Glu	Asn	Phe	Ser	Leu	Ile	Leu
			85					90					95		
Glu	Leu	Ala	Ser	Leu	Ser	Gln	Ser	Ala	Val	Tyr	Phe	Cys	Ala	Ser	Ser
		100					105					110			
Asp	Phe	Ala	Gly	Thr	Gly	Gly	Phe	Tyr	Glu	Gln	Tyr	Phe	Gly	Pro	Gly
	115					120					125				
Thr	Arg	Leu	Thr	Val	Ser										
	130														

<210> 47

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized peptide

<400> 47

Lys	Ile	Phe	Gly	Ser	Leu	Ala	Phe	Leu
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<210> 48

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized peptide

<400> 48

Thr	Leu	Gln	Gly	Leu	Gly	Ile	Ser	Trp	Leu
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<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized peptide

<400> 49
Val Met Ala Gly Val Gly Ser Pro Tyr Val
1 5 10

<210> 50
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized peptide

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Val Leu Gln Gly Leu Pro Arg Glu Tyr Val
1 5 10

<210> 51
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized peptide

<400> 51
His Leu Tyr Gln Gly Gln Gln Trp
1 5

<210> 52
<211> 9
<212> PRT
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<220>
<223> Synthesized peptide

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Arg Leu Leu Gln Glu Thr Glu Leu Val
1 5

<210> 53
<211> 9
<212> PRT
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<220>
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Lys Ile Pro Val Ala Ile Lys Val Leu
1 5

<210> 54
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthesized peptide

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Cys Leu Thr Ser Thr Val Gln Leu Val
1 5

<210> 55

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized peptide

<400> 55

Gln Leu Met Pro Tyr Gly Cys Leu Leu
1 5

<210> 56

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized peptide

<400> 56

Val Leu Val Lys Ser Pro Asn His Val
1 5

<210> 57

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized peptide

<400> 57

Asp Ile Asp Glu Thr Glu Tyr His Ala
1 5

<210> 58

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized peptide

<400> 58

Asp Leu Leu Glu Lys Gly Glu Arg Leu
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<210> 59

<211> 9

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<220>
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<400> 59
Glu Leu Val Ser Glu Phe Ser Arg Met
1 5

<210> 60
<211> 10
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<400> 60
Glu Leu Val Ser Glu Phe Ser Arg Met Ala
1 5 10

<210> 61
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized peptide

<400> 61
Leu Val Ser Glu Phe Ser Arg Met Ala
1 5

<210> 62
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
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<400> 62
Asp Leu Val Asp Ala Glu Glu Tyr Leu
1 5

<210> 63
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized peptide

<400> 63
Thr Leu Ser Pro Gly Lys Asn Gly Val
1 5

<210> 64
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized peptide

<400> 64
Lys Leu Val Gly Lys Leu Asn Trp Ala
1 5

<210> 65
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Flexible linker

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1 5 10 15
Gly Gly Ser Ser Ser
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